



# Blast 2 Sequences results

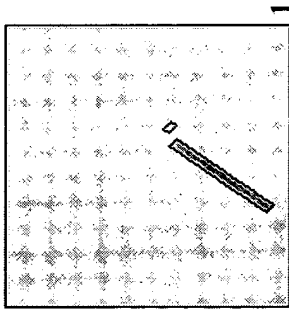
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 lc|seq\_1 Length 8509 (1 .. 8509)

Sequence 2 lc|seq\_2 Length 5859 (1 .. 5859)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3857 bits (2006), Expect = 0.0  
Identities = 2006/2006 (100%)  
Strand = Plus / Plus



Query: 2955 ggcaatgggtcgaaattcatagaaattttgtgtgaggtgcgtagcggctctgacaggggtg 3014

|||||

Sbjct: 402 ggcaatgggtcgaaattcatagaaattttgtgtgaggtgcgtagcggctctgacaggggtg 461

Query: 3015 ctgcgaggagatctctgtgtctcaggtagggcgacaaatggagaggtgttagttgccccctg 3074



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|||||
Sbjct: 462 ctgcgcggagatctctggtctcaggtagggcgacaatggagagggttagttgccccctg 521

Query: 3075 tatcgctctctgcgtggcgcatctgggtcatcctgcccgacatatgatatccgctagag 3134
|||||
Sbjct: 522 tatcgctctctgcgtggcgcatctgggtcatcctgcccgacatatgatatccgctagag 581

Query: 3135 gattactgatatgtttctgcctgtcgggcttgcggcttgcgggcttgcgggcttgtc 3194
|||||
Sbjct: 582 gattactgatatgtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 641

Query: 3195 gggcctgtccctcttgtcccgccctgtccctcactttttcacaaatcaaaaaatgggcgaagc 3254
|||||
Sbjct: 642 gggcctgtccctcttgtcccgccctgtccctcactttttcacaaatcaaaaaatgggcgaagc 701

Query: 3255 ccttcttgttctatagttcttctatagttcatacgaaaaattacacataattatcaatagctt 3314
|||||
Sbjct: 702 ccttcttgttctatagttcttctatagttcatacgaaaaattacacataattatcaatagctt 761

Query: 3315 attcgcttaaaaggaggagtaattggccgcgcaaaaggagtaattggccgcgcaaaaggaggt 3374
|||||
Sbjct: 762 attcgcttaaaaggaggagtaattggccgcgcaaaaggagtaattggccgcgcaaaaggaggt 821

Query: 3375 aattggccgcgcaaaaggaggagtaattggccgcgatatcggttgtttacatggggagggaatcc 3434
|||||
Sbjct: 822 aattggccgcgcaaaaggaggagtaattggccgcgatatcggttgtttacatggggagggaatcc 881

Query: 3435 ccttaatacatcttctcccccatgggaaagacacaacaagtggccgcagaccgggccttcgac 3494
|||||
Sbjct: 882 ccttaatacatcttctcccccatgggaaagacacaacaagtggccgcagaccgggccttcgac 941

Query: 3495 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatcgcgcaatccgccc 3554
|||||
Sbjct: 942 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatcgcgcaatccgccc 1001
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Query: 3555 cgcctgcaggcgctcaagctcatgcatttaatatagccactgcgggcgcgcgatggct 3614  
|||||  
Sbjct: 1002 cgcctgcaggcgctcaagctcatgcatttaatatagccactgcgggcgcgcgatggct 1061

Query: 3615 gatgatgtgcgcccatgaaatcgggctgcccgcacattcgcgcaatcgacggcatgaaaaac 3674  
|||||  
Sbjct: 1062 gatgatgtgcgcccatgaaatcgggctgcccgcacattcgcgcaatcgacggcatgaaaaac 1121

Query: 3675 catgaccgtgagagcctgacccccgctgttcgaggagctagccgctgcgggtgttgacccat 3734  
|||||  
Sbjct: 1122 catgaccgtgagagcctgacccccgctgttcgaggagctagccgctgcgggtgttgacccat 1181

Query: 3735 gatgaccctgcaaaagatgatcgtgacagtcggcggttggtcgcgatgaggcgcgaatagac 3794  
|||||  
Sbjct: 1182 gatgaccctgcaaaagatgatcgtgacagtcggcggttggtcgcgatgaggcgcgaatagac 1241

Query: 3795 taccgccaggaggcaagcggcgaaactcctagtgcgtggaccttcgggagtagacattccgt 3854  
|||||  
Sbjct: 1242 taccgccaggaggcaagcggcgaaactcctagtgcgtggaccttcgggagtagacattccgt 1301

Query: 3855 cgtatggcggcgagtcgaaccactgggccattctcgaccgtcaaaacgggtattccatctc 3914  
|||||  
Sbjct: 1302 cgtatggcggcgagtcgaaccactgggccattctcgaccgtcaaaacgggtattccatctc 1361

Query: 3915 ggtagtaagtattccgtgctgctgttcagcacgctctctagtctcgccaatcttgatcgg 3974  
|||||  
Sbjct: 1362 ggtagtaagtattccgtgctgctgttcagcacgctctctagtctcgccaatcttgatcgg 1421

Query: 3975 atgagcgcgaaaaacctttacggtccccgagttgcgggcgctccttgagtgccccgagggg 4034  
|||||  
Sbjct: 1422 atgagcgcgaaaaacctttacggtccccgagttgcgggcgctccttgagtgccccgagggg 1481

Query: 4035 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 4094  
|||||  
Sbjct: 1482 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1541

Query: 4095 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 4154  
|||||  
Sbjct: 1542 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 1601

Query: 4155 agtgtactataggctgggaagtgaagacgacccaacccgtcgccaggcgagctggcg 4214  
|||||  
Sbjct: 1602 agtgtactataggctgggaagtgaagacgacccaacccgtcgccaggcgagctggcg 1661

Query: 4215 ggttccaaggctcggtcgagatgctcgtcgagaggggcagcggaacgatatagccccctcc 4274  
|||||  
Sbjct: 1662 ggttccaaggctcggtcgagatgctcgtcgagaggggcagcggaacgatatagccccctcc 1721

Query: 4275 ttcccagaagcggggcggtacacctacagtcacgttggtggagctgaaacgctctgct 4334  
|||||  
Sbjct: 1722 ttcccagaagcggggcggtacacctacagtcacgttggtggagctgaaacgctctgct 1781

Query: 4335 ggcagcaacaaggacaaacgatctgatcgccctcagactccggcggtttctgtcgggagaga 4394  
|||||  
Sbjct: 1782 ggcagcaacaaggacaaacgatctgatcgccctcagactccggcggtttctgtcgggagaga 1841

Query: 4395 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagatttctgcgcaaaagta 4454  
|||||  
Sbjct: 1842 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagatttctgcgcaaaagta 1901

Query: 4455 gggaaggtttgagttttgaggtatttcaccgcaatagtggttaaatgactttcgtgaaaacg 4514  
|||||  
Sbjct: 1902 gggaaggtttgagttttgaggtatttcaccgcaatagtggttaaatgactttcgtgaaaacg 1961

Query: 4515 atgtgcaatatagcggtaagactatgaaatcacacggctggacaggctgcataaaagcaaacgg 4574  
|||||  
Sbjct: 1962 atgtgcaatatagcggtaagactatgaaatcacacggctggacaggctgcataaaagcaaacgg 2021

Query: 4575 gtgtggcgaccgcaaccatcactcggcggtctaaaaaagcggtataatttccgggtataaaaaag 4634  
|||||  
Sbjct: 2022 gtgtggcgaccgcaaccatcactcggcggtctaaaaaagcggtataatttccgggtataaaaaag 2081

Query: 4635 atgaatctggggcatgggttatagatcctgcagaattgcacagagtggtttcctcccat 4694  
|||||  
Sbjct: 2082 atgaatctggggcatgggttatagatcctgcagaattgcacagagtggtttcctcccat 2141

Query: 4695 caaagaaatacacaccgaaacacctaacaacgcaagtatatgtgaagcgtgatgaaacacatg 4754  
|||||  
Sbjct: 2142 caaagaaatacacaccgaaacacctaacaacgcaagtatatgtgaagcgtgatgaaacacatg 2201

Query: 4755 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgcctttat 4814  
|||||  
Sbjct: 2202 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgcctttat 2261

Query: 4815 ctgatgccaggaggatcgcgacaaaatggcgcacatggcgcagcgtctttcaatttcat 4874  
|||||  
Sbjct: 2262 ctgatgccaggaggatcgcgacaaaatggcgcacatggcgcagcgtctttcaatttcat 2321

Query: 4875 caccgatgagagaggaagaccgccccctcaaaaaaagatggtggaagatatcttgat 4934  
|||||  
Sbjct: 2322 caccgatgagagaggaagaccgccccctcaaaaaaagatggtggaagatatcttgat 2381

Query: 4935 cctgggcttcaggagccttgccctta 4960  
|||||  
Sbjct: 2382 cctgggcttcaggagccttgccctta 2407

Score = 208 bits (108), Expect = 2e-49  
Identities = 108/108 (100%)  
Strand = Plus / Plus

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Query: 5364 tactggcgaaaaaacgcgatattgaggaagccagggcccgacacttttagaggcggaagccctata 5423  
|||||  
Sbjct: 2406 tactggcgaaaaaacgcgatattgaggaagccagggcccgacacttttagaggcggaagccctata 2465

Query: 5424 acgagtaccacaaacactagaagccagattgaggaataatagggaaacgtg 5471

# Blast Result

|||||  
Sbjct: 2466 acgagtacaaacactagaaagccagattgaggaaaaatagggaacgtg 2513

CPU time: 0.06 user secs. 0.02 sys. secs 0.08 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 1  
Number of Hits to DB: 1061  
Number of extensions: 43  
Number of successful extensions: 14  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 2  
Number of HSP's successfully gapped: 2  
Number of extra gapped extensions for HSPs above 10.0: 0  
Length of query: 8509  
Length of database: 12,527,565,053  
Length adjustment: 28  
Effective length of query: 8481  
Effective length of database: 12,527,565,025  
Effective search space: 106246278977025  
Effective search space used: 106246278977025  
Neighboring words threshold: 0  
Window for multiple hits: 0  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 23 (44.9 bits)